AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions, and listings, of claims in the application.

Listing of Claims:

1. (Currently amended) A method for generating at least one error-corrected experiment profile of at least one experiment profile in a plurality of pairs of profiles $\{A_m, C_m\}$, where m = 1, 2, ..., M, and M is the number of the pairs of profiles; and wherein, for each $m \in \{1, 2, ..., M\}$, A_m is an experiment profile, and C_m is a reference profile; and wherein $\{A_m\}$ represents experiment profiles in said plurality of pairs of profiles $\{A_m, C_m\}$ and $\{C_m\}$ represents reference profiles in said plurality of pairs of profiles $\{A_m, C_m\}$, said method comprising:

(a) calculating an average reference profile $\overline{C}$ of said plurality of reference profiles $\{C_m\}$, where m = 1, 2, ..., M;

(b) determining, for at least one profile pair $\{A_m, C_m\}$ where $m \in \{1, 2, ..., M\}$ of said plurality of pairs of profiles $\{A_m, C_m\}$, a differential reference profile computed between C_m and $\overline{C}$;

(c) adjusting an experiment profile A_m of said at least one profile pair $\{A_m, C_m\}$ where $m \in \{1, 2, ..., M\}$ based on said differential reference profile determined for said profile pair to generate a first error-corrected experiment profile A'_m; for each $m \in \{1, 2, ..., M\}$, <u>wherein</u> said experiment profile A_m comprises a first data set, said reference profile C_m comprises a second data set, said average reference profile $\overline{C}$ comprises data set $\{\overline{C}(k)\}$, and said first error-corrected experiment profile A'_m comprises data set $\{A'_m(k)\}$; wherein said first data set comprises measurements or transformed measurements of a plurality of different cellular constituents measured in a sample having been subject to a first condition ~~of an experiment~~, said second data set comprises measurements or transformed measurements of said plurality of different cellular constituents measured in a sample having been subject to a second condition ~~of said experiment~~; and wherein k = 1, 2, ..., N; k is an index of measurements or transformed measurements of said plurality of different cellular constituents, N being the total number of measurements or transformed measurements; and

(d) outputting to a user interface device, a computer readable storage medium, or a local or remote computer system; or displaying[[;]]: said first error-corrected experiment profile A'_m, said data set $\{A'_m(k)\}$, a second error-corrected experiment profile A''_m, or a data set $\{A''_m(k)\}$, wherein said second error-corrected experiment profile A''_m comprises said data set $\{A''_m(k)\}$ obtained by combining said first error-corrected experiment profile A'_m with said experiment profile A_m using a weighing factor $\{w(k)\}$, k = 1, 2, ..., N, wherein $w(k)$ is a weighing factor for the k'th measurement.

2. (Previously presented) The method of claim 1, wherein said steps (b) and (c) are performed for each profile pair $\{A_m, C_m\}$ where $m \in \{1, 2, \ldots, M\}$.

3. (Previously presented) The method of claim 2, wherein each of said experiment profile A_m and said reference profile C_m comprises measurements or transformed measurements of said plurality of different cellular constituents from the same experimental reaction.

4. (Previously presented) The method of claim 3, wherein said $\overline{C}(k)$ is calculated according to the equation

$$\overline{C}(k) = \frac{1}{M}\sum_{m=1}^{M} C_m(k)$$

wherein said differential reference profile is determined according to the equation

$$C_{diff}(m,k) = C_m(k) - \overline{C}(k)$$

and wherein said first error-corrected experiment profile A'_m is generated according to the equation

$$A'_m(k) = A_m(k) - C_{diff}(m,k)$$

wherein $\{A_m(k)\}$ is said first data set of experiment profile A_m.

5. (Previously presented) The method of claim 4, further comprising

(d) calculating, for each said profile pair $\{A_m, C_m\}$ said second error-corrected experiment profile A''_m; and

(e) outputting to, a user interface device, a computer readable storage medium, or a local or remote computer system; or displaying; said second error-corrected profile A''_m or said data set $\{A''_m(k)\}$.

6. (Previously presented) The method of claim 5, wherein said second error-corrected experiment profile A''_m is calculated according to the equation

$$A''_m(k) = (1 - w(k)) \cdot A_m(k) + w(k) \cdot A'_m(k).$$

7. (Previously presented) The method of claim 6, further comprising determining said weighing factor *w(k)* according to the equation

$$w(k) = 1 - e^{-0.5 \cdot \left(\frac{\bar{C}(k)}{avg\_bkgstd}\right)^2}$$

where *avg_bkgstd* is an average background standard error.

8. (Previously presented) The method of claim 7, further comprising determining said *avg_bkgstd* according to the equation

$$avg\_bkgstd = \frac{1}{N}\sum_{k=1}^{N}\left(\frac{1}{M}\sum_{m=1}^{M} bkgstd(m,k)\right)$$

where *bkgstd (m, k)* is background standard error of $C_m(k)$.

9. (Previously presented) The method of claim 4, further comprising determining errors $\{\sigma'_m(k)\}$ of said data set $\{A'_m(k)\}$ in said first error-corrected experiment profile A'_m.

10. (Previously presented) The method of claim 9, further comprising determining said errors $\{\sigma'_m(k)\}$ according to the equation

$$\sigma'_m(k) = \sqrt{\sigma_m^2(k) + mixed\_\sigma_m^2(k) - 2 \cdot Cor(k) \cdot \sigma_m(k) \cdot mixed\_\sigma_m(k)}$$

where $\sigma_m(k)$ is the standard error of $A_m(k)$, the method further comprising determining $mixed\_\sigma_m(k)$ according to the equation

$$mixed\_\sigma_m(k) = \frac{\sigma_m(k) + (M-1) \cdot \sigma_{ref}(k)}{M}$$

where $\sigma_{ref}(k) = \sqrt{\frac{1}{M-1}\sum_{m}^{M}(C_m(k) - \overline{C}(k))^2}$

and where Cor(k) is a correlation coefficient between said experiment profile A_m and said reference profile C_m.

11. (Previously presented) The method of claim 10, further comprising determining said Cor(k) according to the equation

$$Cor(k) = CorMax \cdot \left(1 - e^{-0.5 \cdot \left(\frac{\overline{C}(k)}{avg\_bkgstd}\right)^2}\right)$$

where CorMax is a number between 0 and 1.

12. (Previously presented) The method of claim 7, further comprising determining errors $\{\sigma''_m(k)\}$ of said data set $\{A''_m(k)\}$ in said second error-corrected experiment profile A''_m.

13. (Previously presented) The method of claim 12, wherein said errors $\{\sigma''_m(k)\}$ are determined according to the equation

$$\sigma''_m(k) = \sqrt{[1 - w(k)] \cdot \sigma_m^2(k) + w(k)\sigma_m'^2(k)}$$

where $\sigma_m(k)$ is the standard error of $A_m(k)$, the method further comprising (i) determining $\sigma'_m(k)$ according to the equation

$$\sigma'_m(k) = \sqrt{\sigma_m^2(k) + mixed\_\sigma_m^2(k) - 2 \cdot Cor(k) \cdot \sigma_m(k) \cdot mixed\_\sigma_m(k)}$$, and

(ii) determining $mixed\_\sigma_m(k)$ according to the equation

$$mixed\_\sigma_m(k) = \frac{\sigma_m(k) + (M-1) \cdot \sigma_{ref}(k)}{M}$$

where $\sigma_{ref}(k) = \sqrt{\frac{1}{M-1}\sum_{m}^{M}(C_m(k) - \overline{C}(k))^2}$

and where Cor(k) is a correlation coefficient between said experiment profile A_m and said reference profile C_m.

14. (Previously presented) The method of claim 13, further comprising determining said Cor(k) according to the equation

$$Cor(k) = CorMax \cdot \left(1 - e^{-0.5\left(\frac{\overline{C}(k)}{avg\_bkgstd}\right)^2}\right)$$

where CorMax is a number between 0 and 1.

15. (Previously presented) The method of claim 2, wherein said experiment profile A_m and said reference profile C_m of each said profile pair $\{A_m, C_m\}$ are measured in a two-channel microarray experiment.

16. (Previously presented) The method of claim 15, wherein said reference profiles $\{C_m\}$, where m = 1, 2, ..., M, are measured with samples labeled with a same label.

17. (Previously presented) The method of claim 2, wherein at least one of said plurality of pairs of profiles $\{A_m, C_m\}$ is a virtual profile.

18. (Currently amended) The method of claim 1, wherein said plurality of pairs of profiles $\{A_m, C_m\}$ are transformed profiles each comprising transformed measurements of said plurality of different cellular constituents in data set ~~$\{TA_m(k)\}$~~ $\underline{\{A_m(k)\}}$ and data set ~~$\{TC_m(k)\}$~~ $\underline{\{C_m(k)\}}$, respectively; and wherein said data set ~~$\{TA_m(k)\}$~~ $\underline{\{A_m(k)\}}$ is said first data set, and said data set ~~$\{TC_m(k)\}$~~ $\underline{\{C_m(k)\}}$ is said second data set.

19 (cancelled).

20. (Previously presented) The method of claim 1, further comprising:

(a0) removing nonlinearity, prior to said calculating step (a), from measurements or transformed measurements of said plurality of different cellular constituents to generate said plurality of pairs of profiles $\{A_m, C_m\}$ comprising said experiment profile A_m and reference profile C_m.

21. (Currently amended) The method of claim 20, wherein said removing step (a0) comprises:

(a0i) calculating an average profile of pre-experiment profiles $\underline{\{A_m^{pre}\}}$ and pre-reference profiles $\underline{\{C_m^{pre}\}}$; wherein each of said pre-experiment profiles comprises measurements or transformed measurements of said plurality of different cellular constituents measured in said sample having been subject to said first condition of said experiment, which when nonlinearity is removed therefrom, produces each said experiment profile A_m; and wherein each of said pre-reference profiles comprises measurements or transformed measurements of said plurality of different cellular constituents measured in said sample having been subject to said second condition of said experiment, which when nonlinearity is removed therefrom, produces each said reference profile C_m; and

(a0ii) adjusting each of said pre-experiment profiles $\underline{\{A_m^{pre}\}}$ based on first differences between each of said pre-experiment profiles $\underline{\{A_m^{pre}\}}$ and said average profile, thereby generating each said experiment profile A_m; and adjusting each of pre-reference profiles $\underline{\{C_m^{pre}\}}$ based on second differences between each of said pre-reference profiles $\underline{\{C_m^{pre}\}}$ and said average profile, thereby generating each said reference profile C_m.

22. (Currently amended) The method of claim 21, further comprising calculating said first differences based on a first subset of said measurements or transformed measurements of said plurality of different cellular constituents in said pre-experiment profiles $\underline{\{A_m^{pre}\}}$ and said average profile; and calculating said second differences based on a second subset of said measurements or transformed measurements of said plurality of different cellular constituents in said pre-reference profiles $\underline{\{C_m^{pre}\}}$ and said average profile.

23. (Currently amended) The method of claim 22, wherein said first subset consists of measurements or transformed measurements of said plurality of different cellular constituents that are ranked similarly between each of said pre-experiment profiles $\underline{\{A_m^{pre}\}}$ and said average profile, and said second subset consists of measurements or transformed measurements of said plurality of different cellular constituents that are ranked similarly between each of said pre-reference profiles $\underline{\{C_m^{pre}\}}$ and said average profile.

24. (Currently amended) The method of claim 23, wherein said adjusting step (a0ii) is carried out by a method comprising:

(ii1) binning said first subset into a first plurality of bins, wherein each of said first plurality of bins consists of measurements or transformed measurements of said plurality of different cellular constituents in one of said pre-experiment profiles $\underline{\{A_m^{pre}\}}$ and said average profile having a value in a given range; and binning said second subset into a second plurality of bins, wherein each of said second plurality of bins consists of measurements or transformed measurements of said plurality of different cellular constituents in one of said pre-reference profiles $\underline{\{C_m^{pre}\}}$ and said average profile having a value in a given range;

(ii2) calculating, in each bin of said first plurality of bins, a first mean difference between a feature value of measurements or transformed measurements of said one of said pre-experiment profiles $\underline{\{A_m^{pre}\}}$ and a feature value of said average profile, and calculating a second mean difference between a feature value of measurements or transformed measurements of said one of said pre-reference profiles $\underline{\{C_m^{pre}\}}$ and a feature value of said average profile;

(ii3) determining a first curve of said first mean difference as a first function of values of measurements or transformed measurements of said plurality of different cellular constituents for said one of said pre-experiment profiles $\underline{\{A_m^{pre}\}}$, wherein said first function is represented by, ~~$nonlinear\_A_m$~~ $\underline{nonlinear\_A_m^{pre}}$; and determining a second curve of said second mean difference as a second function of values of measurements or transformed measurements of said plurality of different cellular constituents for said one of said pre-reference profiles $\underline{\{C_m^{pre}\}}$, wherein said second function is represented by ~~$nonlinear\_C_m$~~ $\underline{nonlinear\_C_m^{pre}}$; and

(ii4) adjusting each of said pre-experiment profiles $\underline{\{A_m^{pre}\}}$ according to the equation:

$$\cancel{A_m^{corr}(k) = A_m(k) - nonlinear\_A_m(k)}$$

$$\underline{A_m(k) = A_m^{pre}(k) - nonlinear\_A_m^{pre}(k)},$$

and adjusting each of said pre-reference profiles $\underline{\{C_m^{pre}\}}$ according to the equation:

$$\cancel{C_m^{corr}(k) = C_m(k) - nonlinear\_C_m(k)}$$

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$\underline{C_m(k) = C_m^{pre}(k) - nonlinear\_C_m^{pre}(k)}$,

where k = 1, …, N; and where ~~{Am(k)}~~ $\underline{A_m^{pre}(k)}$ and ~~{Cm(k)}~~ $\underline{C_m^{pre}(k)}$ are data sets of each of said pre-experiment profiles $\underline{\{A_m^{pre}\}}$ and each of said pre-reference profiles $\underline{\{C_m^{pre}\}}$, respectively; and where ~~$\{A_m^{corr}(k)\}$~~ $\underline{A_m(k)}$ and ~~$\{C_m^{corr}(k)\}$~~ $\underline{C_m(k)}$ are said first data set and said second data set, respectively.

25. (Currently amended) The method of claim 1, further comprising:

(a0) normalizing, prior to said calculating step (a), measurements or transformed measurements of said plurality of different cellular constituents <u>in a pre-experiment profile A_m^{pre} and a pre-reference profile C_m^{pre}</u> to generate said experiment profile A_m and said reference profile C_m<u>, respectively.</u>

26. (Currently amended) The method of claim 25, wherein said normalizing step (a0) comprises normalizing a data set ~~{Am(k)}~~ $\underline{A_m^{pre}(k)}$ and a data set ~~{Cm(k)}~~ $\underline{C_m^{pre}(k)}$, according to the equations:

$$\cancel{NA_m(k) =} \frac{A_m(k) \cdot \overline{AC}}{\overline{A_m}}$$

$$\underline{A_m(k) = \frac{A_m^{pre}(k) \cdot \overline{A_m^{pre} C_m^{pre}}}{\overline{A_m^{pre}}}}$$

and

$$\cancel{NC_m(k) =} \frac{C_m(k) \cdot \overline{AC}}{\overline{C_m}}$$

$$\underline{C_m(k) = \frac{C_m^{pre}(k) \cdot \overline{A_m^{pre} C_m^{pre}}}{\overline{C_m^{pre}}}},$$

wherein said data sets ~~{Am(k)}~~ $\underline{A_m^{pre}(k)}$ and ~~{Cm(k)}~~ $\underline{C_m^{pre}(k)}$ each comprises measurements or transformed measurements of said plurality of different cellular constituents, where ~~$\overline{A_m}$~~ $\underline{\overline{A_m^{pre}}}$ is an average of measurements or transformed measurements of said plurality of different cellular constituents in said ~~{Am(k)}~~ $\underline{A_m^{pre}(k)}$, and ~~$\overline{C_m}$~~ $\underline{\overline{C_m^{pre}}}$ is an average of

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measurements or transformed measurements of said plurality of different cellular constituents in said ~~{C_m(k)}~~ $\underline{C_m^{pre}(k)}$, wherein ~~{NA_m(k)}~~ $\underline{A_m(k)}$ is said first data set, ~~and {NA_m(k)}~~ wherein $\underline{A_m(k)}$ comprises normalized measurements or normalized transformed measurements of said ~~experiment~~ pre-experiment profile ~~A_m~~ $\underline{A_m^{pre}}$; and ~~{NC_m(k)}~~ $\underline{C_m(k)}$ is said second data set~~, and {NC_m(k)}~~ wherein $\underline{A_m(k)}$ comprises normalized measurements or normalized transformed measurements of said reference profile ~~C_m~~ $\underline{C_m^{pre}}$; and wherein ~~$\overline{AC}$~~ $\underline{\overline{A_m^{pre} C_m^{pre}}}$ is an average calculated according to the equation

$$\cancel{\overline{AC} = \frac{1}{2M}\sum_{m=1}^{M}(\overline{A_m} + \overline{C_m})}$$

$$\underline{\overline{A_m^{pre} C_m^{pre}} = \frac{1}{2M}\sum_{m=1}^{M}(\overline{A_m^{pre}} + \overline{C_m^{pre}})}.$$

27. (Currently amended) The method of claim 26, further comprising normalizing errors of said data sets ~~{A_m(k)}~~ $\underline{\{A_m^{pre}(k)\}}$ and ~~{C_m(k)}~~ $\underline{\{C_m^{pre}(k)\}}$, respectively, according to the equations:

$$\cancel{\sigma_m^{NA}(k) =} \frac{\sigma_m^{A}(k)\cdot\overline{AC}}{\overline{A_m}}$$

$$\underline{\sigma_m^{NA}(k) = \frac{\sigma_m^{preA}(k)\cdot\overline{A_m^{pre}C_m^{pre}}}{\overline{A_m^{pre}}}}$$

and

$$\cancel{\sigma_m^{NC}(k) =} \frac{\sigma_m^{C}(k)\cdot\overline{AC}}{\overline{C_m}}$$

$$\underline{\sigma_m^{NC}(k) = \frac{\sigma_m^{preC}(k)\cdot\overline{A_m^{pre}C_m^{pre}}}{\overline{C_m^{pre}}}},$$

where ~~$\sigma_m^A(k)$~~ $\underline{\sigma_m^{preA}(k)}$ and ~~$\sigma_m^C(k)$~~ $\underline{\sigma_m^{preC}(k)}$ are the standard errors of ~~A_m(k)~~ $\underline{A_m^{pre}(k)}$ and ~~C_m(k)~~ $\underline{C_m^{pre}(k)}$, respectively, and $\sigma_m^{NA}(k)$ and $\sigma_m^{NC}(k)$ are normalized standard errors of ~~NA_m(k)~~ $\underline{A_m(k)}$ and ~~NC_m(k)~~ $\underline{C_m(k)}$, respectively.

28. (Currently amended) The method of claim 27, further comprising normalizing background errors of said data sets ~~{Am(k)}~~ $\underline{\{A_m^{pre}(k)\}}$ and ~~{Cm(k)}~~ $\underline{\{C_m^{pre}(k)\}}$, respectively, according to the equations:

$$\cancel{bkgstd_m^{NA}(k) =} \frac{bkgstd_m^{A}(k)\cdot\overline{AC}}{\overline{A_m}}$$

$$\underline{bkgstd_m^{NA}(k) = \frac{bkgstd_m^{preA}(k)\cdot\overline{A_m^{pre}C_m^{pre}}}{\overline{A_m^{pre}}}}$$

and

$$\cancel{bkgstd_m^{NC}(k) =} \frac{bkgstd_m^{C}(k)\cdot\overline{AC}}{\overline{C_m}}$$

$$\underline{bkgstd_m^{NC}(k) = \frac{bkgstd_m^{preC}(k)\cdot\overline{A_m^{pre}C_m^{pre}}}{\overline{C_m^{pre}}}}$$

where $\cancel{bkgstd_m^{A}(k)}$ $bkgstd_m^{preA}(k)$ and $\cancel{bkgstd_m^{C}(k)}$ $\underline{bkgstd_m^{preC}(k)}$ are the standard background errors of ~~Am(k)~~ $\underline{A_m^{pre}(k)}$ and ~~Cm(k)~~ $\underline{C_m^{pre}(k)}$, respectively, and $bkgstd_m^{NA}(k)$ and $bkgstd_m^{NC}(k)$ are normalized standard background errors of ~~NAm(k)~~ $\underline{A_m(k)}$ and ~~NCm(k)~~ $\underline{C_m(k)}$, respectively.

29. (Currently amended) The method of claim 28, further comprising calculating said averages $\cancel{\overline{A_m}}$ $\underline{\overline{A_m^{pre}}}$ and $\cancel{\overline{C_m}}$ $\underline{\overline{C_m^{pre}}}$ by excluding measurements or transformed measurements of said plurality of different cellular constituents having a value among the highest 10% of said measurements or transformed measurements of said plurality of different cellular constituents in said data sets ~~{Am(k)}~~ $\underline{\{A_m^{pre}(k)\}}$ and ~~{Cm(k)}~~ $\underline{\{C_m^{pre}(k)\}}$, respectively.

30. (Currently amended) A method for generating at least one error-corrected experiment profile of at least one experiment profile in a plurality of pairs of profiles $\{XA_m, XC_m\}$, XA_m being an experiment profile, XC_m being a reference profile, where m = 1, 2, … , M, M is the number of pairs of profiles, said method comprising:

(a) processing said plurality of pairs of profiles {XA_m, XC_m} to obtain a plurality of pairs of processed profiles ~~{A_m, C_m}~~{PA_m, PC_m}, ~~A_m~~PA_m being a processed experiment profile, ~~C_m~~PC_m being a processed reference profile;

(b) calculating an average processed reference profile ~~$\bar{C}$~~ $\overline{PC}$ of processed reference profiles ~~{C_m}~~{PC_m}, where m = 1, 2, …, M;

(c) determining, for at least one processed profile pair ~~{A_m, C_m}~~{PA_m, PC_m} where m $\in$ {1, 2, …, M} of said plurality of pairs of processed profiles ~~{A_m, C_m}~~{PA_m, PC_m}, where m = 1, 2, …, M, a differential reference profile computed between ~~C_m~~PC_m and ~~$\bar{C}$~~ $\overline{PC}$;

(d) adjusting a processed experiment profile ~~A_m~~PA_m of said at least one processed profile pair ~~{A_m, C_m}~~{PA_m, PC_m} where m $\in$ {1, 2, …, M} using said differential reference profile determined for said at least one processed profile pair to generate a first error-corrected processed experiment profile ~~A'_m~~ PA'_m; wherein for each m $\in$ {1, 2, …, M}, said processed experiment profile ~~A_m~~PA_m comprises a first processed data set, said processed reference profile ~~C_m~~PC_m comprises a second processed data set, said average processed reference profile ~~$\bar{C}$~~ $\overline{PC}$ comprises data set ~~{$\bar{C}$(k)}~~{$\overline{PC}(k)$}, said first error-corrected processed experiment profile ~~A'_m~~ PA'_m comprises dataset ~~{A'_m(k)}~~{$PA'_m(k)$}, said experiment profile XA_m comprises data set {XA_m(k)}, said reference profile XC_m comprises data set {XC_m(k)}, wherein said data set {XA_m (k)} comprises measurements of a plurality of different cellular constituents measured in a sample having been subject to a first condition, said data set {XC_m(k)} comprises measurements of said plurality of different cellular constituents measured in a sample having been subject to a second condition, and where k = 1, 2, ..., N; k is an index of measurements of cellular constituents, N being the total number of measurements; and

(e) outputting to a user interface device, a computer readable storage medium, or a local or remote computer system; or displaying[[;]]: said first error-corrected processed experiment profile ~~A'_m~~ PA'_m, said data set ~~{A'_m(k)}~~{$PA'_m(k)$}, a second error-corrected processed experiment profile ~~A''_m~~ PA''_m, or a data set ~~{A''_m(k)}~~{$PA''_m(k)$}, wherein said second error-corrected processed experiment profile ~~A''_m~~ PA''_m comprises said data set ~~{A''_m(k)}~~{$PA''_m(k)$} obtained by combining said first error-corrected processed experiment

profile ~~A'm~~ $\underline{PA'_m}$ with said processed experiment profile ~~Am~~$\underline{PA_m}$ using a weighing factor $\{w(k)\}$, k = 1, 2, ..., N, wherein $w(k)$ is a weighing factor for the k'th measurement.

31. (Previously presented) The method of claim 30, wherein said processing step (a) comprises normalizing each said experiment profile XA_m and reference profile XC_m.

32. (Currently amended) The method of claim 31, wherein said normalizing is carried out according to the equations:

$$NA_m(k) = \frac{XA_m(k) \cdot \overline{XAC}}{\overline{XA_m}}$$

and

$$NC_m(k) = \frac{XC_m(k) \cdot \overline{XAC}}{\overline{XC_m}}$$

where $\{NA_m(k)\}$ is said first data set of said processed experiment profile ~~Am~~$\underline{PA_m}$, and $\{NC_m(k)\}$ is said second data set of said processed reference profile ~~Cm~~$\underline{PC_m}$; where $\overline{XA_m}$ is an average of measurements or transformed measurements of said plurality of different cellular constituents of said data set $\{XA_m(k)\}$, and $\overline{XC_m}$ is an average of measurements or transformed measurements of said plurality of different cellular constituents of data set $\{XC_m(k)\}$; and wherein $\overline{XAC}$ is an average calculated according to the equation

$$\overline{XAC} = \frac{1}{2M}\sum_{m=1}^{M}(\overline{XA_m} + \overline{XC_m}).$$

33. (Previously presented) The method of claim 32, further comprising normalizing errors of said experiment profile XA_m and reference profile XC_m according to the equations:

$$\sigma_m^A(k) = \frac{\sigma_m^{XA}(k) \cdot \overline{XAC}}{\overline{XA_m}}$$

and

$$\sigma_m^C(k) = \frac{\sigma_m^{XC}(k) \cdot \overline{XAC}}{\overline{XC_m}}$$

where $\sigma_m^{XA}(k)$ and $\sigma_m^{XC}(k)$ are the standard errors of $XA_m(k)$ and $XC_m(k)$, respectively, and $\sigma_m^{A}(k)$ and $\sigma_m^{C}(k)$ are normalized standard errors of $NA_m(k)$ and $NA_m(k)$, respectively.

34. (Previously presented) The method of claim 33, further comprising normalizing background errors of said experiment profile XA_m and reference profile XC_m according to the equations:

$$bkgstd_m^A(k) = \frac{bkgstd_m^{XA}(k) \cdot \overline{XAC}}{\overline{XA_m}}$$

and

$$bkgstd_m^C(k) = \frac{bkgstd_m^{XC}(k) \cdot \overline{XAC}}{\overline{XC_m}}$$

where $bkgstd_m^{XA}(k)$ and $bkgstd_m^{XC}(k)$ are the standard background errors of $XA_m(k)$ and $XC_m(k)$, respectively, and $bkgstd_m^A(k)$ and $bkgstd_m^C(k)$ are normalized standard background errors of said $NA_m(k)$ and said $NA_m(k)$, respectively.

35. (Previously presented) The method of claim 33, further comprising determining said averages $\overline{XA_m}$ and $\overline{XC_m}$ excluding measurements of said plurality of different cellular constituents having a value among the highest 10% of said measurements or transformed measurements of said plurality of different cellular constituents in said data sets $\{XA_m(k)\}$ and $\{XC_m(k)\}$, respectively.

36. (Currently amended) The method of claim 30, wherein said processing step (a) comprises:

normalizing each said experiment profile XA_m and reference profile XC_m to generate normalized data set $\{NA_m(k)\}$ and normalized data set $\{NC_m(k)\}$, respectively; and

transforming said normalized data set $\{NA_m(k)\}$ to obtain a transformed data set $\{TA_m(k)\}$, where said transformed data set $\{TA_m(k)\}$ is said first data set of said processed experiment profile ~~A_m~~$\underline{PA_m}$; and transforming said normalized data set $\{NC_m(k)\}$ to obtain a transformed data set $\{TC_m(k)\}$, where said transformed data set $\{TC_m(k)\}$ is said second data set of said processed reference profile ~~C_m~~$\underline{PC_m}$.

37. (Previous presented) The method of claim 36, wherein said transforming is carried out according to the equations

$$TA_m(k) = f(x) = \frac{\ln\left(\dfrac{b^2 + 2\cdot a^2 \cdot NA_m(k)}{a} + 2\cdot\sqrt{c^2 + b^2\cdot NA_m(k) + a^2\cdot[NA_m(k)]^2}\right)}{a} + d,$$

for $NA_m(k)>0$

and

$$TC_m(k) = f(x) = \frac{\ln\left(\dfrac{b^2 + 2\cdot a^2 \cdot NC_m(k)}{a} + 2\cdot\sqrt{c^2 + b^2\cdot NC_m(k) + a^2\cdot[NC_m(k)]^2}\right)}{a} + d,$$

for $NC_m(k)>0$

where d is described by the equation

$$d = \frac{-\ln\left(\dfrac{b^2}{a} + 2\cdot c\right)}{a}$$

and where a is the fractional error coefficient of said experiment, b is the Poisson error coefficient of said experiment, and c is the standard deviation of background noise of said experiment.

38. (Previous presented) The method of claim 30, wherein said processing step (a) comprises:

normalizing each said experiment profile XA_m and reference profile XC_m to generate normalized data set $\{NA_m(k)\}$ and normalized data set $\{NC_m(k)\}$, respectively;

transforming said normalized data set $\{NA_m(k)\}$ to obtain a transformed data set $\{TA_m(k)\}$; and transforming said normalized data set $\{NC_m(k)\}$ to obtain a transformed data set $\{TC_m(k)\}$; and

removing nonlinearity from each said transformed data sets $\{TA_m(k)\}$ and $\{TC_m(k)\}$, respectively.

39. (Previous presented) The method of claim 38, wherein said removing nonlinearity is carried out by a method comprising

(a1) calculating an average transformed profile of transformed experiment profiles and transformed reference profiles, wherein each of said transformed experiment profiles contains a corresponding transformed data set $\{TA_m(k)\}$, and each of said transformed reference profiles contains a corresponding transformed data set $\{TC_m(k)\}$; and

(a2) adjusting each of said transformed experiment profiles based on first differences between each of said transformed experiment profiles and said average transformed profile, and adjusting each of said transformed reference profiles based on second differences between each of said transformed reference profiles and said average transformed profile.

40. (Previous presented) The method of claim 39, further comprising calculating said first differences based on the differences in a first subset of transformed measurements of said plurality of different cellular constituents between each of said transformed experiment profiles and said average transformed profile, and calculating said second differences based on the differences in a second subset of transformed measurements of said plurality of different cellular constituents between each of said transformed reference profiles and said average transformed profile.

41. (Previous presented) The method of claim 40, wherein each said first subset consists of transformed measurements that are ranked similarly between each of said transformed experiment profiles and said average transformed profile, and each said second subset consists of transformed measurements that are ranked similarly between each of said transformed reference profiles and said average transformed profile.

42. (Currently amended) The method of claim 41, wherein said adjusting step (a2) is carried out by a method comprising:

(a2i) binning said first subset into a plurality of bins, each said bin consisting of transformed measurements of said plurality of different cellular constituents in one of said transformed experiment profiles and said average transformed profile having a value in a given range; and binning said second subset into a plurality of bins, each said bin consisting of transformed measurements of said plurality of different cellular constituents in one of said transformed reference profiles and said average transformed profile having a value in a given range

(a2ii) calculating, in each bin of said plurality of bins, a first mean difference between a feature value of transformed measurements of said plurality of different cellular constituents in said one of said transformed experiment profiles and a feature value of said average transformed profile, and calculating a second mean difference between a feature

value of transformed measurements of said plurality of different cellular constituents in said one of said reference profiles and a feature value of the average profile;

(a2iii) determining a first curve of said first mean difference as a first function of values of transformed measurements of said plurality of different cellular constituents for said one of said transformed experiment profiles, wherein said first function is represented by, *nonlinear_TA*$_m$, and determining a second curve of said second mean difference as a second function of values of transformed measurements of said plurality of different cellular constituents for said one of said transformed reference profiles, wherein said second function is represented by *nonlinear_TC*$_m$; and

(a2iv) computing corrected transformed measurements of said plurality of different cellular constituents in each said transformed data set $\{TA_m(k)\}$, according to the equation:

$$TA_m^{corr}(k) = TA_m(k) - nonlinear\_TA_m(k),$$

and computing corrected transformed measurements of said plurality of different cellular constituents in each said transformed data set $\{TC_m(k)\}$, according to the equation:

$$TC_m^{corr}(k) = TC_m(k) - nonlinear\_TC_m(k),$$

where k = 1, ..., N; and where $\{TA_m^{corr}(k)\}$ is said first processed data set of said processed experiment profile ~~A_m~~$\underline{PA_m}$, and $\{TC_m^{corr}(k)\}$ is said second processed data set of said processed reference profile ~~C_m~~$\underline{PC_m}$.

43. (Currently amended) The method of claim 42, wherein said processed experiment profile ~~A_m~~$\underline{PA_m}$ and said processed reference profile ~~C_m~~$\underline{PC_m}$ comprise transformed measurements of said plurality of different cellular constituents from the same experimental reaction.

44. (Currently amended) The method of claim 43, further comprising calculating ~~$\overline{C}(k)$~~ $\underline{\overline{PC}(k)}$ according to the equation

$$\cancel{\overline{C}(k) = \frac{1}{M}\sum_{m=1}^{M} C_m(k)}$$

$$\underline{\overline{PC}(k) = \frac{1}{M}\sum_{m=1}^{M} PC_m(k)},$$

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wherein $\cancel{\{C_m(k)\}}$ $\underline{\{PC_m(k)\}}$ comprises transformed measurements from said second processed data set $\{TC_m^{corr}(k)\}$, and calculating said differential reference profile according to the equation

$$\cancel{C_{diff}(m,k) = C_m(k) - \overline{C}(k)}$$

$$\underline{PC_{diff}(m,k) = PC_m(k) - \overline{PC}(k)}$$

and wherein said first error-corrected profile is calculated according to the equation

$$\cancel{A'_m(k) = A_m(k) - C_{diff}(m,k)}$$

$$\underline{PA'_m(k) = PA_m(k) - PC_{diff}(m,k)},$$

wherein $\cancel{\{A_m(k)\}}$ $\underline{\{PA_m(k)\}}$ comprises transformed measurements from said first data set $\{TA_m^{corr}(k)\}$.

45. (Currently amended) The method of claim 44, further comprising

(d) calculating for each processed profile pair ~~{Am, Cm}~~{PAm, PCm}, where $m \in \{1, 2, \ldots, M\}$, a second error-corrected experiment profile ~~A″m~~ $\underline{PA''_m}$ comprising data set ~~{A″m(k)}~~ $\underline{\{PA''_m(k)\}}$ by combining said first error-corrected experiment profile ~~A′m~~ $\underline{PA'_m}$ with said processed experiment profile ~~Am~~PAm using a weighing factor $\{w(k)\}$, k = 1, 2, ..., N, wherein $w(k)$ is a weighing factor for the k' th measurement.

46. (Currently amended) The method of claim 45, wherein said second error-corrected experiment profile ~~A″m~~ $\underline{PA''_m}$ is calculated according to the equation

$$\cancel{A''_m(k) = (1 - w(k)) \cdot A_m(k) + w(k) \cdot A'_m(k)}$$

$$\underline{PA''_m(k) = (1 - w(k)) \cdot PA_m(k) + w(k) PA'_m(k)}.$$

47. (Currently amended) The method of claim 46, further comprising determining said weighing factor according to the equation

$$\cancel{w(k) = 1 - e^{-0.5\left(\frac{\overline{C}(k)}{avg\_bkgstd}\right)^2}}$$

$$\underline{w(k) = 1 - e^{-0.5\left(\frac{\overline{PC}(k)}{avg\_bkgstd}\right)^2}}$$

where *avg_bkgstd* is an average background standard error.

48. (Currently amended) The method of claim 47, further comprising determining said *avg_bkgstd* according to the equation

$$avg\_bkgstd = \frac{1}{N}\sum_{k=1}^{N}\left(\frac{1}{M}\sum_{m=1}^{M} bkgstd(m,k)\right)$$

where *bkgstd (m, k)* is background standard error of ~~$C_m(k)$~~ $PC_m(k)$.

49. (Currently amended) The method of claim 44, further comprising determining errors ~~$\{\sigma'_m\}$~~ $\{P\sigma'_m\}$ of said first error-corrected experiment profile ~~$\{A'_m\}$~~ $\{PA'_m\}$, wherein said ~~$\{\sigma'_m\}$~~ $\{P\sigma'_m\}$ comprises error data set ~~$\{\sigma'_m(k)\}$~~ $\{P\sigma'_m(k)\}$.

50. (Currently amended) The method of claim 49, further comprising determining said error data set ~~$\{\sigma'_m(k)\}$~~ $\{P\sigma'_m(k)\}$ according to the equation

$$\cancel{\sigma'_m(k) = \sqrt{\sigma_m^2(k) + mixed\_\sigma_m^2(k) - 2\cdot Cor(k)\cdot \sigma_m(k)\cdot mixed\_\sigma_m(k)}}$$

$$\sigma'_m(k) = \sqrt{P\sigma_m^2(k) + mixed\_P\sigma_m^2(k) - 2Cor(k)\cdot P\sigma_m(k)\cdot mixed\_P\sigma_m(k)}$$

where ~~$\sigma_m(k)$~~ $P\sigma_m(k)$ is the standard error of $A_m(k)$, and determining ~~$mixed\_\sigma_m(k)$~~ $mixed\_P\sigma_m(k)$ according to the equation

$$\cancel{mixed\_\sigma_m(k) =} \frac{\sigma_m(k) + (M-1)\cdot\sigma_{ref}(k)}{M}$$

$$mixed\_P\sigma_m(k) = \frac{P\sigma_m(k) + (M-1)\cdot P\sigma_{ref}(k)}{M}$$

where $\cancel{\sigma_{ref}(k) = \sqrt{\frac{1}{M-1}\sum_m^M (C_m(k) - \overline{C}(k))^2}}$

$$P\sigma_{ref}(k) = \sqrt{\frac{1}{M-1}\sum_m^M (PC_m(k) - \overline{PC}(k))^2}$$

and where Cor(k) is a correlation coefficient between said processed experiment profile ~~A_m~~ PA_m and said processed reference profile ~~C_m~~ PC_m.

51. (Currently amended) The method of claim 50, wherein said Cor(k) is determined according to the equation

$$\cancel{Cor(k) = CorMax \cdot \left(1 - e^{-0.5\cdot\left(\frac{\overline{C}(k)}{avg\_bkgstd}\right)^2}\right)}$$

$$\underline{Cor(k) = CorMax \cdot \left(1 - e^{-0.5\left(\frac{\overline{PC}(k)}{avg\_bkgstd}\right)^2}\right)}$$

where CorMax is a number between 0 and 1.

52. (Currently amended) The method of claim 51, further comprising determining errors $\cancel{\{\sigma''_m\}}\{\underline{P\sigma''_m}\}$of said second error-corrected experiment profile ~~{A''_m}~~$\{\underline{PA''_m}\}$, wherein said $\cancel{\{\sigma''_m\}}\{\underline{P\sigma''_m}\}$comprises error data set $\cancel{\{\sigma''_m(k)\}}\{\underline{P\sigma''_m(k)}\}$.

53. (Currently amended) The method of claim 52, further comprising determining said error data set $\cancel{\{\sigma''_m(k)\}}\{\underline{P\sigma''_m(k)}\}$ according to the equation

$$\cancel{\sigma''_m(k) = \sqrt{[1-w(k)]\cdot\sigma^2_m(k) + w(k)\sigma'^2_m(k)}}$$

$$\underline{P\sigma''_m(k) = \sqrt{[1-w(k)]\cdot P\sigma^2_m(k) + w(k)P\sigma'^2_m(k)}}$$

where $\cancel{\sigma_m(k)}\ \underline{P\sigma_m(k)}$ is the standard error of $\cancel{A_m(k)}\ \underline{PA_m(k)}$, and <u>further comprising</u> determining $\cancel{\sigma'_m(k)}\ \underline{P\sigma'_m(k)}$ according to the equation

$$\cancel{\sigma'_m(k) = \sqrt{\sigma^2_m(k) + mixed\_\sigma^2_m(k) - 2\cdot Cor(k)\cdot\sigma_m(k)\cdot mixed\_\sigma_m(k)}}$$

$$\underline{P\sigma'_m(k) = \sqrt{P\sigma^2_m(k) + mixed\_P\sigma^2_m(k) - 2\cdot Cor(k)\cdot P\sigma_m(k)\cdot mixed\_P\sigma_m(k)}}$$, and

further comprising determining $\cancel{mixed\_\sigma_m(k)}\ \underline{mixed\_P\sigma_m(k)}$ according to the equation

$$\cancel{mixed\_\sigma_m(k) = \frac{\sigma_m(k) + (M-1)\cdot\sigma_{ref}(k)}{M}}$$

$$\underline{mixed\_P\sigma_m(k) = \frac{P\sigma_m(k) + (M-1)\cdot P\sigma_{ref}(k)}{M}}$$

where $\cancel{\sigma_{ref}(k) = \sqrt{\frac{1}{M-1}\sum_{m}^{M}(C_m(k) - \overline{C}(k))^2}}$

$$\underline{P\sigma_{ref}(k) = \sqrt{\frac{1}{M-1}\sum_{m}^{M}(PC_m(k) - \overline{PC}(k))^2}}$$

and where Cor(k) is a correlation coefficient between said processed experiment profile ~~A_m~~$\underline{PA_m}$ and said processed reference profile ~~C_m~~$\underline{PC_m}$.

54. (Currently amended) The method of claim 53, further comprising determining said Cor(k) according to the equation

$$\cancel{Cor(k) = CorMax \cdot \left(1 - e^{-0.5\cdot\left(\frac{\overline{C}(k)}{avg\_bkgstd}\right)^2}\right)}$$

$$\underline{Cor(k) = CorMax \cdot \left(1 - e^{-0.5\left(\frac{\overline{PC}(k)}{avg\_bkgstd}\right)^2}\right)}$$

where CorMax is a number between 0 and 1.

55. (Previously presented) The method of claim 54, wherein each said pair of profiles XA_m and XC_m comprise measurements of said plurality of different cellular constituents from a two-channel microarray experiment.

56. (Previously presented) The method of claim 55, wherein said reference profiles $\{XC_m\}$, m = 1, 2, ... , M, are measured with samples labeled with a same label.

57. (Previously presented) The method of claim 56, wherein at least one of said pairs of profiles $\{XA_m, XC_m\}$ is a virtual profile.

58. (Previously presented) A computer system comprising

a processor, and

a memory coupled to said processor and encoding one or more programs,

wherein said one or more programs cause the processor to carry out the method of any one of claims 1-18 and 20-57.

59. (Previously presented) A computer program product for use in conjunction with a computer having a processor and a memory connected to the processor, said computer program product comprising a computer readable storage medium having a computer program mechanism encoded thereon, wherein said computer program mechanism may be loaded into the memory of said computer and cause said computer to carry out the method of any one of claims 1-18 and 20-57.

60. (Withdrawn) A method for generating a differential profile A vs. B from differential profiles A vs. C_A and B vs. C_B, comprising calculating said differential profile A vs. B according to equation

$$lratioAB(k) = polarityAC \cdot lratioAC(k) - polarityBC \cdot lratioBC(k)$$

where $k = 1, 2, \ldots,$ N, is the index of measurements in a profile, N being the total number of measurements; wherein $lratioAC(k) = \text{Log}\{A(k) / C_A(k)\}$, if $PolarityAC = 1$, and $lratioAC(k) = \text{Log}\{ C_A(k) / A(k)\}$, if $PolarityAC = -1$, where $A(k)$, and $C_A(k)$ are the k'th measurement from sample A and C_A, respectively; wherein $lratioBC(k) = \text{Log}\{B(k) / C_B(k)\}$, if $PolarityBC = 1$, and $lratioAC(k) = \text{Log}\{ C_B(k) / B(k)\}$, if $PolarityBC = -1$, where $B(k)$, and $C_B(k)$ are the k'th measurement from sample B and C_B, respectively; wherein {A(k)} representing measurements of a plurality of different cellular constituents measured in a sample having been subject to condition A, {B(k)} representing measurements of said plurality of different cellular constituents measured in a sample having been subject to condition B, and $\{C_A(k)\}$ and $\{C_B(k)\}$ each representing measurements of said plurality of different cellular constituents measured in a sample having been subject to condition C.

61. (Withdrawn) The method of claim 60, further comprising calculating an error of differential profile A vs. B according to equation

$$\sigma_{lratioAB}(k) = \sqrt{\sigma^2_{lratioAC}(k) + \sigma^2_{lratioBC}(k) - 2 \cdot CorMax \cdot \sigma_{lratioAC}(k) \cdot \sigma_{lratioBC}(k)}$$

wherein $\sigma_{lratioAC}(k)$ and $\sigma_{lratioBC}(k)$ are errors of $lratioAC(k)$ and $lratioBC(k)$, respectively, and wherein CorMax is an estimated maximum correlation coefficient between errors of A/C and B/C.

62. (Withdrawn) The method of claim 60, wherein A vs. C_A and B vs. C_B are experimentally measured profiles.

63. (Withdrawn) The method of claim 60, wherein at least one of A vs. C_A and B vs. C_B is a virtual profile.

64. (Withdrawn) A computer system comprising

a processor, and

a memory coupled to said processor and encoding one or more programs,

wherein said one or more programs cause the processor to carry out the method of any one of claims 60-63.

65. (Withdrawn) A computer program product for use in conjunction with a computer having a processor and a memory connected to the processor, said computer program product comprising a computer readable storage medium having a computer program mechanism encoded thereon, wherein said computer program mechanism may be loaded into the memory of said computer and cause said computer to carry out the method of any one of claims 60-63.

66. (Currently amended) A method for generating at least one error-corrected experiment profile of at least one experiment profile A_m, where $m \in \{1, 2, \ldots, M\}$ in at least one of a plurality of pairs of profiles $\{A_m, C_m\}$, A_m being an experiment profile, C_m being a reference profile, where $m = 1, 2, \ldots, M$, M is the number of pairs of profiles, said method comprising:

adjusting said experiment profile A_m using a differential reference profile calculated between C_m and an average reference profile $\overline{C}$ determined for said profile pair $\{A_m, C_m\}$ where $m \in \{1, 2, \ldots, M\}$ to generate an error-corrected experiment profile A'_m; wherein said average reference profile $\overline{C}$ is an average of reference profiles $\{C_m\}$, $m = 1, 2, \ldots, M$; wherein for each $m \in \{1, 2, \ldots, M\}$, said error-corrected experiment profile A'_m comprises data set $\{A'_m(k)\}$, said experiment profile A_m comprises data set $\{A_m(k)\}$, said reference profile C_m comprises data set $\{C_m(k)\}$, and said average reference profile $\overline{C}$ comprises data set $\{\overline{C}(k)\}$, wherein said data set $\{A_m(k)\}$ comprises measurements or transformed measurements of a plurality of different cellular constituents measured in a sample having been subject to a first condition, said data set $\{C_m(k)\}$ comprises measurements or

transformed measurements of said plurality of different cellular constituents measured in a sample having been subject to a second condition, wherein k = 1, 2, ..., N; k is an index of measurements or transformed measurements of cellular constituents, N being the total number of measurements; and

outputting to, a user interface device, a computer readable storage medium, or a local or remote computer system; or displaying[[;]]: said first error-corrected profile A'_m, said data set $\{A'_m(k)\}$, a second error-corrected profile A''_m, or a data set $\{A''_m(k)\}$, wherein said second error-corrected profile A''_m comprises said data set $\{A''_m(k)\}$ obtained by combining said first error-corrected experiment profile A'_m with said experiment profile A_m using a weighing factor $\{w(k)\}$, k = 1, 2, ..., N, wherein $w(k)$ is a weighing factor for the k'th measurement.

67. (Currently amended) The method of claim 18, further comprising obtaining said transformed measurements of said ~~$\{TA_m(k)\}$~~ data set $\{A_m(k)\}$ and said ~~$\{TC_m(k)\}$~~ data set $\{C_m(k)\}$ according to the equations:

$$\cancel{TA_m(k) = f(x) = \frac{\ln\left(\frac{b^2 + 2 \cdot a^2 \cdot XA_m(k)}{a}\right) + 2 \cdot \sqrt{c^2 + b^2 \cdot XA_m(k) + a^2 \cdot [XA_m(k)]^2}}{a} + d}$$

$$A_m(k) = f(x) = \frac{\ln\left(\frac{b^2 + 2 \cdot a^2 \cdot XA_m(k)}{a}\right) + 2 \cdot \sqrt{c^2 + b^2 \cdot XA_m(k) + a^2 \cdot [XA_m(k)]^2}}{a} + d,$$

for $XA_m(k) > 0$

and

$$\cancel{TC_m(k) = f(x) = \frac{\ln\left(\frac{b^2 + 2 \cdot a^2 \cdot XC_m(k)}{a} + 2 \cdot \sqrt{c^2 + b^2 \cdot XC_m(k) + a^2 \cdot [XC_m(k)]^2}\right)}{a} + d}$$

$$C_m(k) = f(x) = \frac{\ln\left(\frac{b^2 + 2 \cdot a^2 \cdot XC_m(k)}{a} + 2 \cdot \sqrt{c^2 + b^2 \cdot XC_m(k) + a^2 \cdot [XC_m(k)]^2}\right)}{a} + d,$$

for $XC_m(k) > 0$

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where $\{XA_m(k)\}$ and $\{XC_m(k)\}$ are data sets comprising measurements of said plurality of different cellular constituents that when transformed produce said transformed measurements of said plurality of different cellular constituents of said ~~$\{TA_m(k)\}$~~ data set $A_m(k)$ and said ~~$\{TC_m(k)\}$~~ data set $C_m(k)$, respectively, where d is described by the equation:

$$d = \frac{-\ln\left(\frac{b^2}{a} + 2 \cdot c\right)}{a}$$

and where a is the fractional error coefficient of said experiment, b is the Poisson error coefficient of said experiment, and c is the standard deviation of background noise of said experiment.

68. (Previously presented) A computer system comprising

a processor, and

a memory coupled to said processor and encoding one or more programs,

wherein said one or more programs cause the processor to carry out the method of claim 66 or 67.

69. (Previously presented) A computer program product for use in conjunction with a computer having a processor and a memory connected to the processor, said computer program product comprising a computer readable storage medium having a computer program mechanism encoded thereon, wherein said computer program mechanism may be loaded into the memory of said computer and cause said computer to carry out the method of claim 66 or 67.

70. (Previously presented) The method of claim 30, wherein said processing comprises:

normalizing, transforming, and /or removing nonlinearity from measurements of said plurality of cellular constituents of said data set $\{XA_m(k)\}$of said experiment profile XA_m, and from measurements of said plurality of cellular constituents of said data set $\{XC_m(k)\}$of said reference profile XC_m.